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0003013616
The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus
pneumoniae: Functional and Structural Correlation
Nieto, Concha; Cherny, Izhack; Khoo, Seok Kooi; de Lacoba, Mario Garcia; Chan, Wai Ting; Yeo, Chew Chieng; Gazit, Ehud; Espinosa, Manuel Centro de Investigaciones Biologicas, CSIC, Madrid, Spain. Department of Molecular Microbiology and Biotechnology, Tel Aviv University, Tel Aviv 69978, Israel. Department of
Biotechnology, Malaysia University of Science and Technology, Petaling Jaya,
Journal of Bacteriology , v 189 , n 4 , p 1266	ext{-}1278 , February 2007
Publication Date: 2007
Publisher: American Society for Microbiology, 1752 N Street N.W. Washington, DC
20036 USA, [URL:http://www.asm.org/]
Document Type: Journal Article
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Summary Language: English
ISSN: 0021-9193
Electronic Issn: 1098-5530
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The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus
pneumoniae: Functional and Structural Correlation
Nieto, Concha; Cherny, Izhack; Khoo, Seok Kooi; de Lacoba, Mario Garcia; Chan, Wai
Ting; Yeo, Chew Chieng; Gazit...
Abstract:
Toxin-antitoxin loci belonging to the yefM-yoeB family are located in the chromosome or in some....We cloned the yefM-yoeB locus of Streptococcus pneumoniae, and these genes encode bona fide antitoxin (YefM sub(Spn)) and toxin (YoeB sub(Spn)) products. We showed that overproduction of YoeB......K-12 strains. The YoeB
sub(Spn)-mediated toxicity could be reversed by the cognate antitoxin, YefM
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proteins were purified and were shown to interact with each other both in vitro and
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in vivo. Far-UV circular dichroism analyses indicated that the pneumococcal

antitoxin was partially, but not totally, unfolded and was different than its E. coli counterpart. Molecular... ...whereas the antitoxins appeared to be specifically designed for each bacterial locus; thus, the toxin-antitoxin interactions were adapted to the different bacterial environmental conditions. Both structural features, folding and the...

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The YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

Cherny, Izhack; Rockah, Liat; Gazit, Ehud Department of Molecular Microbiology and Biotechnology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel

Aviv 69978, Israel Journal of Biological Chemistry , v 280 , n 34 , p 30063-30072 , August 2005

Publication Date: 2005

Publisher: American Society for Biochemistry and Molecular Biology, 9650 Rockville Pike Bethesda MD 20814-3996 USA, [mailto:asbmb@asbmb.faseb.org],

[URL:http://www.jbc.org]

Document Type: Journal Article

Record Type: Abstract Language: English

Summary Language: English ISSN: 0021-9258

Electronic Issn: 1083-351X

File Segment: Bacteriology Abstracts (Microbiology B); Genetics Abstracts ...YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

Cherny, Izhack; Rockah, Liat; Gazit, Ehud

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The YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

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Pike Bethesda MD 20814-3996 USA, [mailto:asbmb@asbmb.faseb.org],

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Nieto, Concha; Cherny, Izhack; Khoo, Seok Kooi; de Lacoba, Mario Garcia; Chan, Wai Ting; Yeo, Chew Chieng; Gazit, Ehud; Espinosa, Manuel Centro de Investigaciones Biologicas, CSIC, Madrid, Spain. Department of Molecular Microbiology and Biotechnology, Tel Aviv University, Tel Aviv 69978, Israel. Department of Biotechnology, Malaysia University of Science and Technology, Petaling Jaya, Journal of Bacteriology , v 189 , n 4 , p 1266-1278 , February 2007 Publication Date: 2007 Publisher: American Society for Microbiology, 1752 N Street N.W. Washington, DC 20036 USA, [URL:http://www.asm.org/]

Document Type: Journal Article

Record Type: Abstract Language: English

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File Segment: Bacteriology Abstracts (Microbiology B)

The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus

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Cherny, Izhack; Rockah, Liat; Gazit, Ehud Department of Molecular Microbiology and Biotechnology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978, Israel Journal of Biological Chemistry , v 280 , n 34 , p 30063-30072 , August 2005 Publication Date: 2005 Publisher: American Society for Biochemistry and Molecular Biology, 9650 Rockville Pike Bethesda MD 20814-3996 USA, [mailto:asbmb@asbmb.faseb.org], [URL:http://www.jbc.org]

Document Type: Journal Article

Record Type: Abstract Language: English

toxin-antitoxin systems

Summary Language: English ISSN: 0021-9258

Electronic Issn: 1083-351X

File Segment: Bacteriology Abstracts (Microbiology B)

...YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

Cherny, Izhack; Rockah, Liat; Gazit, Ehud

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chromatography implying the formation of a YoeB.YefM complex. The unstable antitoxin was removed from the mixture by natural proteolysis, and the residual YoeB protein was purifiedthermal unfolding at temperatures up to 56 degree C. The thermodynamic features of the toxin-antitoxin complex were similar. Taken together, our results support the notion of a correlation between differential physiological and structural stability in toxin- antitoxin modules.

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0001838986 IP Accession No: 6517911
The YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

Cherny, Izhack; Rockah, Liat; Gazit, Ehud Department of Molecular Microbiology and Biotechnology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978, Israel

Journal of Biological Chemistry , v 280 , n 34 , p 30063-30072 , August 2005

Publication Date: 2005

Publisher: American Society for Biochemistry and Molecular Biology, 9650 Rockville Pike Bethesda MD 20814-3996 USA, [mailto:asbmb@asbmb.faseb.org], [URL:http://www.jbc.org]

Document Type: Journal Article

Record Type: Abstract Language: English

Summary Language: English ISSN: 0021-9258 Electronic Issn: 1083-351X

File Segment: Bacteriology Abstracts (Microbiology B)

...YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

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General Sci Abs
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6009748 H.w. Wilson Record Number: BGSA07151710
Structural and Thermodynamic Characterization of the Escherichia coli RelBE
Toxin-Antitoxin System: Indication for a Functional Role of Differential Stability

Cherny, Izhack Overgaard, Martin; Borch, Jonas Biochemistry (American Chemical Society) v. 46 no43 (October 30 2007) p. 12152-63 Document Type: Feature Article Special Features: Bibliographic Footnote Graph Illustration Table ISSN: 0006-2960 Language: English Country Of Publication: United States Structural and Thermodynamic Characterization of the Escherichia coli RelBE Toxin-Antitoxin System: Indication for a Functional Role of Differential Stability Cherny, Izhack 4/3,K/8 (Item 2 from file: 98) Links General Sci Abs (c) 2009 The HW Wilson Co. All rights reserved. H.w. Wilson Record Number: BGSA07109307 The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus pneumoniae: Functional and Structural Correlation Nieto, Concha Cherny, Izhack; Khoo, Seok Kooi Journal of Bacteriology v. 189 no4 (February 2007) p. 1266-78 Document Type: Feature Article Special Features: Bibliography Graph Illustration Table ISSN: 0021-9193 Language: English Country Of Publication: United States The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus pneumoniae: Functional and Structural Correlation Cherny, Izhack... 4/3,K/9 (Item 1 from file: 143) Links Biol. & Agric. Index (c) 2009 The HW Wilson Co. All rights reserved. H.W. Wilson Record Number: BBAI07163431 Structural and Thermodynamic Characterization of the Escherichia coli RelBE Toxin-Antitoxin System: Indication for a Functional Role of Differential Stability Cherny, Izhack Overgaard, Martin; Borch, Jonas Biochemistry (American Chemical Society) v. 46 no43 (October 30 2007) p. 12152-63 ISSN: 0006-2960 Structural and Thermodynamic Characterization of the Escherichia coli RelBE Toxin-Antitoxin System: Indication for a Functional Role of Differential Stability Cherny, Izhack 4/3,K/10 (Item 2 from file: 143) Links Biol. & Agric. Index (c) 2009 The HW Wilson Co. All rights reserved. H.W. Wilson Record Number: BBAI07110528 The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus pneumoniae: Functional and Structural Correlation Nieto, Concha Cherny, Izhack; Khoo, Seok Kooi Journal of Bacteriology v. 189 no4 (February 2007) p. 1266-78 ISSN: 0021-9193 The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus pneumoniae: Functional and Structural Correlation Cherny, Izhack...

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4/3,K/11 (Item 3 from file: 143) Links
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           H.W. Wilson Record Number: BBAI05152088
The YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded
YefM Antitoxin. Implications for a Structural-based Differential Stability of
Toxin-antitoxin Systems
Cherny, Izhack
Rockah, Liat; Gazit, Ehud
The Journal of Biological Chemistry v. 280 no34 (August 26 2005) p. 30063-72 ISSN: 0021-9258
 ...YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded
YefM Antitoxin. Implications for a Structural-based Differential Stability of
Toxin-antitoxin Systems
Cherny, Izhack
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           H.W. Wilson Record Number: BBAI04118529
The YefM Antitoxin Defines a Family of Natively Unfolded Proteins: Implications as a
Novel Antibacterial Target
Cherny, Izhack
Gazit, Ehud
The Journal of Biological Chemistry v. 279 no9 (Feb. 27 2004) p. 8252-61 Document Type: Feature Article ISSN: 0021-9258
The YefM Antitoxin Defines a Family of Natively Unfolded Proteins: Implications as a
Novel Antibacterial Target
Cherny, Izhack
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                  CA: 147(25)516306m
                                              JOURNAL
Structural and Thermodynamic Characterization of the Escherichia coli RelBE
Toxin-Antitoxin System: Indication for a Functional Role of Differential Stability
Author: Cherny, Izhack; Overgaard, Martin; Borch, Jonas; Bram, Yaron; Gerdes, Kenn;
Gazit, Ehud
Location: Department of Molecular Microbiology and Biotechnology, George S. Wise
Faculty of Life Sciences, Tel Aviv University, 69978, Tel Aviv-Jaffa, Israel
Journal: Biochemistry
Date: 2007
Volume: 46 Number: 43 Pages: 12152-12163
CODEN: BICHAW
ISSN: 0006-2960
Publisher Item Identifier: 0006-2960(70)01037-1
Language: English
Publisher: American Chemical Society
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antitoxintoxin.txt
Bacterial toxin-antitoxin systems as targets for the development of novel
antibiotics
Author: Alonso, Juan C.; Balsa, Dolors; Cherny, Izhack; Christensen, Susanne K.;
Espinosa, Manuel; Francuski, Djordje; Gazit, Ehud; Gerdes, Kenn; Hitchin, Ed; Martin, M. Teresa; Nieto, Concepcion; Overweg, Karin; Pellicer, Teresa; Saenger, Wolfram; Welfle, Heinz; Welfle, Karin; Wells, Jerry Location: Department of Microbial Biotechnology, Centro Nacional de Biotecnologia,
CSIC, Madrid, Spain, 28049
Journal: Enzyme-Mediated Resist. Antibiot.
Editor: Bonomo, Robert A. (Ed), Tolmasky, Marcelo (Ed),
Date: 2007
Pages: 313-329
CODEN: 69JIC6
Language: English
Publisher: American Society for Microbiology , Washington, D. C
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                     CA: 146(11)200059w
                                                      JOURNAL
The yefM-yoeB toxin-antitoxin systems of Escherichia coli and Streptococcus
pneumoniae: functional and structural correlation
Author: Nieto, Concha; Cherny, Izhack; Khoo, Seok Kooi; Garcia de Lacoba, Mario;
Chan, Wai Ting; Yeo, Chew Chieng; Gazit, Ehud; Espinosa, Manuel
Location: Centro de Investigaciones Biologicas, CSIC, Madrid, Spain,
Journal: J. Bacteriol.
Date: 2007
Volume: 189 Number: 4 Pages: 1266-1278
CODEN: JOBAAY
ISSN: 0021-9193
Language: English
Publisher: American Society for Microbiology
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                                                     JOURNAL
The YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded
YefM Antitoxin: implications for a structural-based differential stability of
toxin-antitoxin systems
Author: Cherny, Izhack; Rockah, Liat; Gazit, Ehud
Location: George S. Wise Faculty of Life Sciences, Department of Molecular
Microbiology and Biotechnology, Tel Aviv University, 69978, Tel Aviv-Jaffa, Israel
Journal: J. Biol. Chem.
Date: 2005
Volume: 280 Number: 34 Pages: 30063-30072
CODEN: JBCHA3
ISSN: 0021-9258
Language: English
Publisher: American Society for Biochemistry and Molecular Biology
 4/3,K/17 (Item 5 from file: 399) Links
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PATENT

Page 9

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CA: 142(20)367629m

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antitoxintoxin.txt
Antibacterial agents disrupting toxin-antitoxin binding and methods of identifying
and utilizing such agents
Inventor (Author): Gazit, Ehud; Cherny, Izhack
Location: Israel
Assignee: Ramot at Tel Aviv University Ltd.
Patent: PCT International; WO 200531362 A2 Date: 20050407
Application: WO 2004IL898 (20040927) *US 2003PV507488 (20031002) *US 2004PV550334
(20040308)
Pages: 108 pp.
CODEN: PIXXD2
Language: English
Patent Classifications:
  class:
             G01N-033/68A
Designated Countries: AE; AG; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BW; BY; BZ; CA;
CH; ČN; CO; CR; CU; CZ; ĎE; ĎK; ĎM; ĎZ; ÉC; ÉE; ÉG; ÉS; ÉI; ĞB; ĞD; ĞE; ĞH; ĞM; ĤR;
HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MA; MD; MG;
MK; MN; MW; MX; MZ; NA; NI; NO; NZ; OM; PG; PH; PL; PT; RO; RU; SC; SD; SE; SG; SK;
SL: SY: TJ: TM: TN: TR: TT: TZ: UA: UG: US: UZ: VC: VN: YU: ZA: ZM: ZW
Designated Regional: BW; GH; GM; KE; LS; MW; MZ; NA; SD; SL; SZ; TZ; UG; ZM; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM; AT; BE; BG; CH; CY; CZ; DE; DK; EE; ES; FI; FR; GB;
GR; HU; IE; IT; LU; MC; NL; PL; PT; RO; SE; SI; SK; TR; BF; BJ; CF; CG; CI; CM; GA; GN; GQ; GW; ML; MR; NE; SN; TD; TG
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140334320
                                                   JOURNAL
The YefM Antitoxin Defines a Family of Natively Unfolded Proteins: Implications as a
Novel Antibacterial Target
Author: Cherny, Izhack; Gazit, Ehud
Location: George S. Wise Faculty of Life Sciences, Department of Molecular
Microbiology and Biotechnology, Tel-Aviv University, 69978, Tel-Aviv, Israel
Journal: J. Biol. Chem.
Date: 2004
Volume: 279 Number: 9 Pages: 8252-8261
CODEN: JBCHA3
ISSN: 0021-9258
Language: English
Publisher: American Society for Biochemistry and Molecular Biology
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Structural and thermodynamic characterization of the Escherichia coli RelBE
toxin-antitoxin system: Indication for a functional role of differential stability
Cherny, Izhack; Overgaard, Martin; Borch, Jonas; Bram, Yaron; Gerdes, Kenn; Gazit,
Ehud
 Corresp. Author/Affil: Gazit, E.: Department of Molecular Microbiology and
Biotechnology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel
Aviv 69978, Israel
 Corresp. Author email: ehudg@post.tau.ac.il
Biochemistry ( Biochemistry ) ( United States ) 2007 46/43 (12152-12163)
 Publication Date: 20071030
 Publisher: American Chemical Society
  CODEN: BICHA
                   ISSN: 0006-2960
Item Identifier (DOI): 10.1021/bi701037e
                                            Page 10
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Document Type: Article; Journal Record Type: Abstract

Treatment: L; (Literature review); X; (Experimental)

Language: English Summary Language: English

Number of References: 63

Structural and thermodynamic characterization of the Escherichia coli RelBE toxin-antitoxin system: Indication for a functional role of differential stability

Cherny, Izhack; Overgaard, Martin; Borch, Jonas; Bram, Yaron; Gerdes, Kenn; Gazit,

The RelE and RelB proteins constitute the RNA interferase (toxin) and its cognate inhibitor (antitoxin) components of the Escherichia coli relBE toxin-antitoxin system. Despite the well-described functionality and physiological activity of this system in E. coli... ...components from E. coli in solution, both separately and in their complexed state. The RelB antitoxin, an alpha-helical protein according to circular dichroism and infrared spectroscopy, forms oligomers in solution... Descriptors:

4/3, K/20 (Item 2 from file: 8) Links

Fulltext available through: STIC Full Text Retrieval Options

Ei Compendex(R)

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0016688330 E.I. COMPENDEX No: 2005369345704
The YoeB toxin is a folded protein that forms a physical complex with the unfolded YefM antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

Cherny, Izhack; Rockah, Liat; Gazit, Ehud

Corresp. Author/Affil: Gazit, E.: Dept. of Molecular Microbiology and

Biotechnology, Tel Aviv University, Tel Aviv 69978, Israel Corresp. Author email: ehudg@post.tau.ac.il Journal of Biological Chemistry (J. Biol. Chem.) (United States) 2005 280/34 (30063 - 30072)

Publication Date: 20050826

Publisher: American Society for Biochemistry and Molecular Biology Inc.

ISSN: 0021-9258 CODEN: JBCHA

Item Identifier (DOI): 10.1074/jbc.M506220200

Document Type: Article; Journal Record Type: Abstract

Treatment: X; (Experimental)

Summary Language: English Language: English

Number of References: 55

..YoeB toxin is a folded protein that forms a physical complex with the unfolded YefM antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

Cherny, Izhack; Rockah, Liat; Gazit, Ehud

The chromosomal YoeB-YefM toxin-antitoxin module common to numerous strains of bacteria is presumed to have a significant role in survival under stringent conditions. Recently we showed that the purified YefM antitoxin is a natively unfolded protein, as we previously reported for the Phd antitoxin in the P1 phage Doc-Phd toxin-antitoxin system. Here we report the purification and structural properties of the YoeB toxin and present.....Q-Sepharose ion-exchange chromatography implying the formation of a YoeB-YefM complex. The unstable antitoxin was removed from the mixture by natural proteolysis, and the residual YoeB protein was purifiedthermal unfolding at temperatures up to 56 (deg)C. The thermodynamic features of the toxin-antitoxin complex were similar. Taken together, our results support the notion of a correlation between differential physiological and structural stability in toxin- antitoxin modules. (c) 2005 by The American Society for Biochemistry and Molecular Biology, Inc. Descriptors:

Identifiers: Antitoxin; Conformational stability; Ion exchange chromatography; Structural stability

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4/3,K/21 (Item 3 from file: 8)
                                        Links
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                                         STIC Full Text Retrieval Options
Ei Compendex(R)
(c) 2009 Elsevier Eng. Info. Inc. All rights reserved. 0015854420 E.I. COMPENDEX No: 2004128066957
0015854420
The YefM antitoxin defines a family of natively unfolded proteins: Implications as a
novel antibacterial target
Cherny, Izhack; Gazit, Ehud
Corresp. Author/Affil: Gazit, E.: Dept. of Molec. Microbiol./Biotech., Tel-Aviv
University, Green Bldg., Ramat-Aviv, Tel-Aviv 69978, Israel
Corresp. Author email: ehudg@post.tau.ac.il
Journal of Biological Chemistry ( J. Biol. Chem. ) ( United States ) 2004 279/9
(8252 - 8261)
 Publication Date: 20040227
 Publisher: American Society for Biochemistry and Molecular Biology Inc.
                     ISSN: 0021-9258
  CODEN: JBCHA
Item Identifier (DOI): 10.1074/jbc.M308263200
 Document Type: Article; Journal
Treatment: T; (Theoretical)
Language: English Summary Lang
                                            Record Type: Abstract
 Language: English Summary Language: English Number of References: 32
The YefM antitoxin defines a family of natively unfolded proteins: Implications as a
novel antibacterial target
Cherny, Izhack; Gazit, Ehud
...well understood. Here, we demonstrate that the Escherichia coli YefM protein is a natively unfolded antitoxin, lacking secondary structure even at low temperature or in the presence of a stabilizing agent ... ... Indeed, a pair-constrained bioinformatic analysis facilitated the definite determination of novel YefM-YoeB
toxin-antitoxin systems in a large number of bacteria including major pathogens such
as Staphylococcus aureus, Streptococcus...
 Descriptors:
 4/3,K/22 (Item 1 from file: 149) Links
TGG Health&wellness DB(SM)
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03335715 Supplier Number: 163707106 (USE FORMAT 7 OR 9 FOR FULL TEXT )
The yefM-yoeB toxin-antitoxin systems of Escherichia coli and Streptococcus
pneumoniae: functional and structural correlation (Author abstract)
Nieto, Concha; Cherny, Izhack; Khoo, Seok Kooi; de Lacoba, Mario Garcia; Chan, Wai
Ting; Yeo, Chew Chieng; Gazit, Ehud; Espinosa, Manuel Journal of Bacteriology , 189 , 3-4 , 1266(13)
Feb , 2007
Document Type: Author abstract Publication Format: Magazine/Journal
ISSN: 0021-9193
Language: English
Record Type: Abstract Target Audience: Academic
The yefM-yoeB toxin-antitoxin systems of Escherichia coli and Streptococcus
pneumoniae: functional and structural correlation (Author abstract)
...Cherny, Izhack
Author Abstract: Toxin-antitoxin loci belonging to the yefM-yoeB family are located
in the chromosome or in some... ... We cloned the yefM-yoeB locus of Streptococcus
pneumoniae, and these genes encode bona fide antitoxin (Yef(M.sub.Spn)) and toxin
Yoe(B.sub.Spn)-mediated toxicity could be reversed by the cognate antitoxin,
Yef(M.sub.Spn), but not by overproduction of the E. coli YefM antitoxin. The
                                                Page 12
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pneumococcal proteins were purified and were shown to interact with each other both in vitro and in vivo. Far-UV circular dichroism analyses indicated that the pneumococcal antitoxin was partially, but not totally, unfolded and was different than its E. coli counterpart. Molecular....whereas the antitoxins appeared to be specifically designed for each bacterial locus; thus, the toxin-antitoxin interactions were adapted to the different bacterial environmental conditions. Both structural features, folding and the...

Text:

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          Items
                   Description
                   S E1-E4
S1
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S2
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 8/3,K/1 (Item 1 from file: 24) Links
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0003502673
                  IP Accession No: 8820610
Crystallization of Doc and the Phd-Doc toxin-antitoxin complex
Garcia-Pino, Abel; Dao-Thi, Minh-Hoa; Gazit, Ehud; Magnuson, Roy David; Wyns, Lode; Loris, Remy Laboratorium voor Ultrastructuur, Vrije Universiteit Brussel, Pleinlaan 2, B-1050 Brussel, Belgium, [mailto:agarciap@vub.ac.be] Acta Crystallographica Section F , v 64 , n 11 , p 1034-1038 , November 1, 2008
Publication Date: 2008
Publisher: Blackwell Publishing Ltd., 9600 Garsington Road
Document Type: Journal Article
Record Type: Abstract
Language: English
Summary Language: English
ISSN: 1744-3091
File Segment: Bacteriology Abstracts (Microbiology B)
Crystallization of Doc and the Phd-Doc toxin-antitoxin complex
Garcia-Pino, Abel; Dao-Thi, Minh-Hoa; Gazit, Ehud; Magnuson, Roy David; Wyns, Lode;
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Loris, Remy

Abstract:

...its plasmidic form in Escherichia coli and is the archetype of a family of bacterial toxin-antitoxin modules. The His66Tyr mutant of Doc (Doc super(H66Y)) was crystallized in space group...

8/3,K/2 (Item 2 from file: 24) Links

Fulltext available through: STIC Full Text Retrieval Options

CSA Life Sciences Abstracts

(c) 2009 CSA. All rights reserved. 0003013616 IP Accession No: 7288149 The yefm-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus pneumoniae: Functional and Structural Correlation

Nieto, Concha; Cherny, Izhack; Khoo, Seok Kooi; de Lacoba, Mario Garcia; Chan, Wai Ting; Yeo, Chéw Chieng; Gazit, Ehud; Espinosa, Manuel Centro de Investigacionés Biologicas, CSIC, Madrid, Spain. Department of Molecular Microbiology and Biotechnology, Tel Aviv Úniversity, Tel Aviv 69978, Israel. Department of Biotechnology, Malaysia University of Science and Technology, Petaling Jaya, Malaysia

Journal of Bacteriology , v 189 , n 4 , p 1266-1278 , February 2007

Publication Date: 2007

Publisher: American Society for Microbiology, 1752 N Street N.W. Washington, DC

20036 USA, [URL:http://www.asm.org/]

Document Type: Journal Article

Record Type: Abstract

Language: English Summary Language: English ISSN: 0021-9193

Electronic Issn: 1098-5530

File Segment: Bacteriology Abstracts (Microbiology B)

The yefM-yoeB Toxin-Antitoxin Systems of Escherichia coli and Streptococcus

pneumoniae: Functional and Structural Correlation

...Cherny, Izhack; Khoo, Seok Kooi; de Lacoba, Mario Garcia; Chan, Wai Ting; Yeo, Chew Chieng; Gazit, Ehud; Espinosa, Manuel

Abstract:

Toxin-antitoxin loci belonging to the yefM-yoeB family are located in the chromosome or in....locus of Streptococcus pneumoniae, and these genes encode bona fide antitoxin (YefM sub(Spn)) and toxin (YoeB sub(Spn)) products. We showed that overproduction of YoeB sub(Spn) is toxic to....homologous, whereas the antitoxins appeared to be specifically designed for each bacterial locus; thus, the toxin-antitoxin interactions were adapted to the different bacterial environmental conditions. Both structural features, folding and...

8/3,K/3 (Item 3 from file: 24) Links

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CSA Life Sciences Abstracts

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IP Accession No: 6517911 0002893868

The YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems

Cherny, Izhack; Rockah, Liat; Gazit, Ehud Department of Molecular Microbiology and Biotechnology, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Page 14

antitoxintoxin.txt Aviv 69978, Israel Journal of Biological Chemistry , v 280 , n 34 , p 30063-30072 , August 2005 Publication Date: 2005 Publisher: American Society for Biochemistry and Molecular Biology, 9650 Rockville Pike Bethesda MD 20814-3996 USA, [mailto:asbmb@asbmb.faseb.org], [URL:http://www.jbc.org] Document Type: Journal Article Record Type: Abstract Language: English Summary Language: English ISSN: 0021-9258 Electronic Issn: 1083-351X File Segment: Bacteriology Abstracts (Microbiology B); Genetics Abstracts
The YoeB Toxin Is a Folded Protein That Forms a Physical Complex with the Unfolded
YefM Antitoxin: Implications for a structural-based differential stability of toxin-antitoxin systems Cherny, Izhack; Rockah, Liat; Gazit, Ehud Abstract: The chromosomal YoeB-YefM toxin-antitoxin module common to numerous strains of bacteria is presumed to have a significant role....protein, as we previously reported for the Phd antitoxin in the P1 phage Doc-Phd toxin-antitoxin system. Here we report the purification and structural properties of the YoeB toxin and present physical evidence for the existence of a tight YoeB. YefM polypeptide complex in... ...physical complex between the proteins. Near- and far-UV circular dichroism spectroscopy of the purified toxin revealed that, similar to the Doc toxin, YoeB is a well-folded protein. Thermal denaturation experiments confirmed the conformational stability of the YoeB toxin, which underwent reversible thermal unfolding at temperatures up to 56 degree C. The thermodynamic features of the toxin-antitoxin complex were similar. Taken together, our results support the notion of a correlation between differential physiological and structural stability in toxin-antitoxin modules.

Identifiers: YoeB toxin; YoeM toxin
Subj Catg:

8/3,K/4 (Item 1 from file: 50) Links Fúlltext available through: STIC Full Text Retrieval Options CAB Abstracts (c) 2009 CAB International. All rights reserved. CAB Accession Number: 20043072465 The role of Bacillus thuringiensis Cry1C and Cry1E separate structural domains in the interaction with Spodoptera littoralis gut épithelial cells. Avisar, D.; Keller, M.; Gazit, E.; Prudovsky, E.; Sneh, B.; Zilberstein, A. Author email address: aviah@post.tau.ac.il
Department of Plant Sciences, George S. Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978, Israel.

Journal of Biological Chemistry vol. 279 (16): p.15779-15786 Publication Year: 2004 ISSN: 0021-9258 Digital Object Identifier: 10.1074/jbc.M312597200 Publisher: American Society for Biochemistry and Molecular Biology Inc Bethesda . Language: English Record Type: Abstract Document Type: Journal article ... and lower K SUB d than Cry1C domain II and further supported the existence of toxin multisite interactions. Competitive binding assays were used to estimate the sequence of interaction events. Cry1C... three domains specifically interact with the epithelial cell membrane. The folding of the three-domain toxin probably

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antitoxintoxin.txt
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dictates the sequence of interaction events.

'umbrella-like" structure of the pore.

8/3,K/6 (Item 3 from file: 50)

Avisar, D.; Keller, M.; Gazit, E.; Prudovsky, E.; Sneh, B.; Zilberstein, A.

8/3,K/5 (Item 2 from file: 50) Links
Fulltext available through: STIC Full Text Retrieval Options
CAB Abstracts
(c) 2009 CAB International. All rights reserved.
0007654000 CAB Accession Number: 19981112254
The structure and organization within the membrane of the helices composing the pore-forming domain of Bacillus thuringiensis delta-endotoxin are consistent with an

Gazit, E.; Rocca, P. la; Sansom, M. S. P.; Shai, Y.
Department of Biological Chemistry, Weizmann Institute of Science, Rehovot, 76100, Israel.
Proceedings of the National Academy of Sciences of the United States of America vol. 95 (21): p.12289-12294
Publication Year: 1998
ISSN: 0027-8424
Language: English Record Type: Abstract
Document Type: Journal article
... The relative affinities for membranes of peptides corresponding to the seven helices that compose the toxin pore-forming domain, their modes of membrane interaction, their structures within membranes, and their orientations...

Gazit, E.; Rocca, P. la; Sansom, M. S. P.; Shai, Y.

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CAB Abstracts
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0007590985 CAB Accession Number: 19980504640
Bacillus thuringiensis cytolytic toxin associates specifically with its synthetic helices A and C in the membrane bound state. Implications for the assembly of oligomeric transmembrane pores.

Links

Gazit, E.; Burshtein, N.; Ellar, D. J.; Sawyer, T.; Shai, Y.
Department of Membrane Research and Biophysics, Weizmann Institute of Science, Rehovot 76100, Israel.
Biochemistry (Washington) vol. 36 (49): p.15546-15554
Publication Year: 1997
ISSN: 0006-2960
Language: English Record Type: Abstract
Document Type: Journal article
Bacillus thuringiensis cytolytic toxin associates specifically with its synthetic helices A and C in the membrane bound state. Implications...
... corresponding to beta5, beta6, and beta7 strands, to a conserved nonhelical region of the CytA toxin of B. thuringiensis subsp. israeliensis (P SUP 149-170), to helices B and D, and..... 149-170 and helix D bind the membrane weakly.
Membrane permeation experiments suggested that CytA toxin exerts its activity by aggregation of several monomers. To learn about the structural elements that..... the membrane. Taken together, these results provide further support for the suggestion that the CytA toxin self-assembles within membrane and that helices A and C are major structural elements involved in the membrane interaction and intermolecular assembly of the toxin.

Gazit, E.; Burshtein, N.; Ellar, D. J.; Sawyer, T.; Shai, Y.

8/3,K/7 (Item 4 from file: 50) Links

Fulltext available through: STIC Full Text Retrieval Options CAB Abstracts (c) 2009 CAB International. All rights reserved. CAB Accession Number: 19950500311 0006949830 Structural characterization, membrane interaction, and specific antibody assembly within phospholipid membranes of hydrophobic segments from Bacillus thuringiensis var. israelensis cytolytic toxin. Gazit, E.; Shai, Y. Department of Mémbrane Research and Biophysics, Weizmann Institute of Science, Rehovot 76100, Israel. Biochemistry (washington) vol. 32 (46): p.12363-12371 Publication Year: 1993 ISSN: 0006-2960 Language: English Record Type: Abstract Document Type: Journal article ... specific antibody assembly within phospholipid membranes of hydrophobic segments from Bacillus thuringiensis var. israelensis cytolytic toxin.
The B. thuringiensis subsp. israelensis (Bti) cytolytic toxin is hypothesized to exert its toxic activity via pore formation in the cell membrane as a result of the aggregation of several monomers. To gain insight into the toxin's mode of action, 2 putative hydrophobic 22 amino acid peptides were synthesized and characterized...helix-2), and the other to amino acids 50-71 (termed helix-1) of the toxin. Circular dichroism spectroscopy revealed that both segments adopt high alpha-helical content in the hydrophobic......for helices-1 and -2 in the assembly and in the pore formation by Bti toxin. Gazit, E.; Shai, Y. 8/3,K/8 (Item 1 from file: 98) Links General Sci Abs (c) 2009 The HW Wilson Co. All rights reserved. H.w. Wilson Record Number: BGSI98058148 The structure and organization within the membrane of the helices composing the pore-forming domain of Bacillus thuringienesis d-endotoxin are consistent with an 'umbrella-like" structure of the pore. Gazit, Ehud La Rocca, Paolo; Sansom, Mark S. P Proceedings of the National Academy of Sciences of the United States of America (Proc Natl Acad Sci U S A) v. 95 no21 (Oct. 13 '98) p. 12289-94 Special Features: bibl il ISSN: 0027-8424 Language: English Country Of Publication: United States Gazit, Ehud Abstract: ...the results suggest an "umbrella" model for the structure of the pores formed by the toxin. The findings also support previous suggestions that the a'h helix may function as the binding... Descriptors: Bacillus thuringiensis toxin: Membrane fusion 8/3,K/9 (Item 2 from file: 98) Links General Sci Abs (c) 2009 The HW Wilson Co. All rights reserved. H.w. Wilson Record Number: BGSI94004244 Structural characterization, membrane interaction, and specific assembly within

phospholipid membranes of hydrophobic segments from Bacillus thuringiensis var.

israelensis cytolytic toxin.

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Gazit, Ehud
Shai, Yechiel
Biochemistry (American Chemical Society) (Biochemistry) v. 32 (Nov. 23 '93) p.
Document Type: Feature Article
Special Features: bibl il
                               ISSN: 0006-2960
Language: English
Country Of Publication: United States
...and specific assembly within phospholipid membranes of hydrophobic segments from
Bacillus thuringiensis var. israelensis cytolytic toxin.
Gazit, Ehud
Abstract: The Bacillus thuringiensis var. israelensis (Bti) cytolytic toxin is
hypothesized to exert its toxic activity via pore formation in the cell membrane as
a result of the aggregation of several monomers. To gain insight into the toxin's
mode of action, 2 putative hydrophobic 22 amino acid peptides were synthesized and characterized.....Ellar, D. J., & Chilcott, C. N. (1988) J. Mol. Biol. 202, 527-535} of the toxin. Circular dichroism spectroscopy revealed that both segments
adopt high a-helical content in a hydrophobic... ...for helices-1 and -2 in the
assembly and in the pore formation by Bti toxin. Copyright 1993, American Chemical
Society. .
Descriptors:
Bacillus thuringiensis toxin; Membranes (Biology...
 8/3, K/10 (Item 3 from file: 98) Links
General Sci Abs
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             H.w. Wilson Record Number: BGSI93014029
Structural and functional characterization of the a5 segment of Bacillus
thuringiensis d-endotoxin.
Gazit, Ehud
Shai, Yechiel
Biochemistry (American Chemical Society) (Biochemistry) v. 32 (Apr. 6'93) p.
Document Type: Feature Article
Special Features: bibl il ISS
                               ISSN: 0006-2960
Language: English
Country Of Publication: United States
Gazit, Ehud
Descriptors:
Bacillus thuringiensis toxin; Proteins...
 8/3,K/11 (Item 1 from file: 143) Links
Biol. & Agric. Index
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            H.W. Wilson Record Number: BBAI99041346
The Doc toxin and Phd antidote proteins of the bacteriophage P1 plasmid addiction
system form a heterotrimeric complex
Gazit, Ehud
Sauer, Robert T
The Journal of Biological Chemistry v. 274 no24 (June 11 1999) p. 16813-18 Document Type: Feature Article ISSN: 0021-9258
The Doc toxin and Phd antidote proteins of the bacteriophage P1 plasmid addiction
system form a heterotrimeric complex
Gazit, Ehud
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8/3,K/12 (Item 1 from file: 399) Links
                                        STIC Full Text Retrieval Options
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(c) 2009 American Chemical Society. All rights reserved.
                     CA: 147(25)516306m
                                                      JOURNAL
Structural and Thermodynamic Characterization of the Escherichia coli RelBE
Toxin-Antitoxin System: Indication for a Functional Role of Differential Stability
Author: Cherny, Izhack; Overgaard, Martin; Borch, Jonas; Bram, Yaron; Gerdes, Kenn;
Location: Department of Molecular Microbiology and Biotechnology, George S. Wise
Faculty of Life Sciences, Tel Aviv University, 69978, Tel Aviv-Jaffa, Israel Journal: Biochemistry
Date: 2007
Volume: 46 Number: 43 Pages: 12152-12163
CODEN: BICHAW
ISSN: 0006-2960
Publisher Item Identifier: 0006-2960(70)01037-1
Language: English
Publisher: American Chemical Society
 8/3,K/13 (Item 2 from file: 399) Links
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147482564
                     CA: 147(23)482564b
                                                      CONFERENCE PROCEEDING
Bacterial toxin-antitoxin systems as targets for the development of novel
antibiotics
Author: Alonso, Juan C.; Balsa, Dolors; Cherny, Izhack; Christensen, Susanne K.; Espinosa, Manuel; Francuski, Djordje; Gazit, Ehud; Gerdes, Kenn; Hitchin, Ed; Martin, M. Teresa; Nieto, Concepcion; Overweg, Karin; Pellicer, Teresa; Saenger, Wolfram; Welfle, Heinz; Welfle, Karin; Wells, Jerry Location: Department of Microbial Biotechnology, Centro Nacional de Biotecnologia,
CSIC, Madrid, Spain, 28049
Journal: Enzyme-Mediated Resist. Antibiot.
Editor: Bonomo, Robert A. (Ed), Tolmasky, Marcelo (Ed),
Date: 2007
Pages: 313-329
CODEN: 69JIC6
Language: English
Publisher: American Society for Microbiology , Washington, D. C
 8/3,K/14 (Item 3 from file: 399) Links
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142367629
                     CA: 142(20)367629m
                                                      PATENT
Antibacterial agents disrupting toxin-antitoxin binding and methods of identifying
and utilizing such agents
Inventor (Author): Gazit, Ehud; Cherny, Izhack
Location: Israel
Assignee: Ramot at Tel Aviv University Ltd.
Patent: PCT International; WO 200531362 A2 Date: 20050407
Application: WO 2004IL898 (20040927) *US 2003PV507488 (20031002) *US 2004PV550334
(20040308)
Pages: 108 pp.
CODEN: PIXXD2
Language: English
Patent Classifications:
  class:
             G01N-033/68A
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antitoxintoxin.txt
Designated Countries: AE; AG; AL; AM; AT; AU; AZ; BA; BB; BG; BR; BW; BY; BZ; CA;
CH; CN; CO; CR; CU; CZ; DE; DK; DM; DZ; EC; EE; EG; ES; FI; GB; GD; GE; GH; GM; HR;
HU; ID; IL; IN; IS; JP; KE; KG; KP; KR; KZ; LC; LK; LR; LS; LT; LU; LV; MA; MD; MG;
MK; MN; MW; MX; NA; NI; NO; NZ; OM; PG; PH; PL; PT; RO; RU; SC; SD; SE; SG; SK; SL; SY; TJ; TM; TN; TT; TZ; UA; UG; US; UZ; VC; VN; YU; ZA; ZM; ZW Designated Regional: BW; GH; GM; KE; LS; MW; MZ; NA; SD; SL; SZ; TZ; UG; ZM; ZW; AM; AZ; BY; KG; KZ; MD; RU; TJ; TM; AT; BE; BG; CH; CY; CZ; DE; DK; EE; ES; FI; FR; GB; GR; HU; IE; IT; LU; MC; NL; PL; PT; RO; SE; SI; SK; TR; BF; BJ; CF; CG; CI; CM; GA;
GN; GQ; GW; ML; MR; NE; SN; TD; TG
 8/3,K/15 (Item 4 from file: 399) Links
    Fulltext available through: STIC Full Text Retrieval Options
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140334320
                    CA: 140(21)334320j
The YefM Antitoxin Defines a Family of Natively Unfolded Proteins: Implications as a
Novel Antibacterial Target
Author: Cherny, Izhack; Gazit, Ehud
Location: George S. Wise Faculty of Life Sciences, Department of Molecular
Microbiology and Biotechnology, Tel-Aviv University, 69978, Tel-Aviv, Israel
Journal: J. Biol. Chem.
Date: 2004
Volume: 279 Number: 9 Pages: 8252-8261
CODEN: JBCHA3
ISSN: 0021-9258
Language: English
Publisher: American Society for Biochemistry and Molecular Biology
 8/3,K/16 (Item 5 from file: 399) Links
    Fulltext available through:
                                       STIC Full Text Retrieval Options
CA SEARCH(R)
(c) 2009 American Chemical Society. All rights reserved.
                    CA: 130(5)48562q
130048562
                                                  JOURNAL
The structure and organization within the membrane of the helixes composing the
pore-forming domain of Bacillus thuringiensis .delta.-endotoxin are consistent with an "umbrella-like" structure of the pore
Author: Gazit, Ehud; La Rocca, Paolo; Sansom, Mark S. P.; Shai, Yechiel
Location: Department of Biological Chemistry, Weizmann Institute of Science, 76100,
Rehovot, Israel
Journal: Proc. Natl. Acad. Sci. U. S. A.
Date: 1998
Volume: 95 Number: 21 Pages: 12289-12294
CODEN: PNASA6
ISSN: 0027-8424
Language: English
Publisher: National Academy of Sciences
 8/3,K/17 (Item 6 from file: 399) Links
    Fulltext available through:
                                       STIC Full Text Retrieval Options
CA SEARCH(R)
(c) 2009 American Chemical Society. All rights reserved.
128044828 CA: 128(5)44828s JOURNAL Bacillus thuringiensis Cytolytic Toxin Associates Specifically with Its Synthetic
Helixes A and C in the Membrane Bound State. Implications for the Assembly of
Oligomeric Transmembrane Pores
Author: Gazit, Ehud; Burshtein, Noga; Ellar, David J.; Sawyer, Trevor; Shai. Yechiel
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antitoxintoxin.txt
Location: Department of Membrane Research and Biophysics, Weizmann Institute of
Science, 76100, Rehovot, Israel
Journal: Biochemistry
Date: 1997
Volume: 36 Number: 49 Pages: 15546-15554
CODEN: BICHAW
ISSN: 0006-2960
Publisher Item Identifier: 0006-2960(97)00758-7
Language: English
Publisher: American Chemical Society
 8/3,K/18 (Item 7 from file: 399) Links
CA SEARCH(R)
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123027507
                  CA: 123(3)27507r
                                            CONFERENCE PROCEEDING
Membrane interaction and hemolytic activity of the .alpha.5 helix of
.delta.-endotoxin
Author: Gazit, Ehut; Shai, Yechiel
Location: Department Membrane Research and Biophysics, Weizmann Institute Science
Rehovot, 76100, Israel
Journal: Recent Adv. Mol. Biochem. Res. Proteins, Proc. IUBMB Symp. Protein Struct.
Funct.
Editor: Wei, Yau-huei (Ed), Chen, Ching-san (Ed), Su, Jong-ching (Ed),
Date: 1993
Pages: 145-53
CODEN: 61HNAL
Language: English
Meeting Date: 920000
Publisher: World Sci. , Singapore, Singapore
 8/3,K/19 (Item 8 from file: 399) Links
   Fulltext available through:
                                   STIC Full Text Retrieval Options
CA SEARCH(R)
(c) 2009 American Chemical Society. All rights reserved.
122003545 CA: 122(1)3545e JOURNAL The alpha.-5 segment of Bacillus thuringiensis delta.-endotoxin: in vitro
activity, ion channel formation and molecular modeling
Author: Gazit, Ehud; Bach, Diana; Kerr, Ian D.; Sansom, Mark S. P.; Chejanovsky,
Nor; Shai, Yechiel
Location: Dep. Membrane Res. Biophys., Weizmann Inst. Sci., 76100, Rehovot, Israel
Journal: Biochem. J.
Date: 1994
Volume: 304 Number: 3 Pages: 895-902
CODEN: BIJOAK
ISSN: 0264-6021
Language: English
 8/3,K/20 (Item 9 from file: 399) Links
   Fulltext available through:
                                   STIC Full Text Retrieval Options
CA SEARCH(R)
(c) 2009 American Chemical Society. All rights reserved.
118163181 CA: 118(17)163181d JOURNAL Structural and functional characterization of the .alpha.5 segment of Bacillus
thuringiensis .delta.-endotoxin
Author: Gazit, Ehud; Shai, Yechiel
Location: Dep. of Membrane Res. Biophys., Weizmann Inst. Sci., 76100, Rehovot,
Israel
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Journal: Biochemistry

Date: 1993

Volume: 32 Number: 13 Pages: 3429-36

CODEN: BICHAW ISSN: 0006-2960 Language: English

8/3,K/21 (Item 1 from file: 185) Links

STIC Full Text Retrieval Options Fulltext available through:

Zoological Record Online(R)

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04966596 BIOSIS No. 14008048631
The role of Bacillus thuringiensis Cry1C and Cry1E separate structural domains in the interaction with Spodoptera littoralis gut epithelial cells.

Authors: Avisar, Dror; Keller, Menahem; Gazit, Ehud; Prudovsky, Evgenia; Sneh,

Baruch; Zilberstein, Áviah (a) Authors Address: (a) Tel Aviv Univ, George S Wise Fac Life Sci, IL-69978 Tel Aviv;

Israel aviah@post.tau.ac.il

Source: Journal of Biological Chemistry 279(16), April 16 2004: 15779-15786. [Print]

Document Type: Article ISSN: 0021-9258

Languages: English Summary Languages: English

Record Type: Abstract

Authors: Avisar, Dror; Keller, Menahem; Gazit, Ehud; Prudovsky, Evgenia; Sneh,

Baruch; Zilberstein, Aviah...

Abstract: ...higher Bmax and lower Kd than Cry1C domain II and further supported the existence of toxin multisite interactions. Competitive binding assays were used to estimate the sequence of interaction events. Cry1C....three domains specifically interact with the epithelial cell membrane. The folding of the three-domain toxin probably dictates the sequence of interaction events.

8/3,K/22 (Item 1 from file: 149) Links

TGG Health&wellness DB(SM)

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03335715 Supplier Number: 163707106 (USE FORMAT 7 OR 9 FOR FULL TEXT)
The yefM-yoeB toxin-antitoxin systems of Escherichia coli and Streptococcus pneumoniae: functional and structural correlation. (Author abstract)

Nieto, Concha; Cherny, Izhack; Khoo, Seok Kooi; de Lacoba, Mario Garcia; Chan, Wai

Ting; Yeo, Chéw Chieng; Gazit, Ehud; Espinosa, Manuel Journal of Bacteriology, 189, 3-4, 1266(13)

Feb

2007

Document Type: Author abstract Publication Format: Magazine/Journal ISSN: 0021-9193

Language: English

Record Type: Abstract Target Audience: Academic

The yefM-yoeB toxin-antitoxin systems of Escherichia coli and Streptococcus

pneumoniae: functional and structural correlation.(Author abstract)

...Gazit, Ehud

Author Abstract: Toxin-antitoxin loci belonging to the yefM-yoeB family are located in the chromosome or in....of Streptococcus pneumoniae, and these genes encode bona fide antitoxin (Yef(M.sub.Spn)) and toxin (Yoe(B.sub.Spn)) products. We showed that overproduction of Yoe(B.sub.Spn),, is....homologous, whereas the antitoxins appeared to be specifically designed for each bacterial locus; thus, the toxin-antitoxin interactions were adapted to the different bacterial environmental conditions. Both structural features, folding and...

Text:

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Set	Items	Description
S1	276	S E1-E4
s2	42	S S1 AND TOXIN
S 3	28	S E1-E3
S4 S5	22	S S3 AND ANTITOXIN
S5	42	S S2
s6	42	S S5 AND TOXIN
S7	42	S S6 AND TOXIN
S8	22	RD (unique items)